Applicants regard as the invention. The amendments in claims 1, 3, 4, and 5 are fully supported by the specification, *inter alia*, on page 5, lines 6-18; page 11, line 19 to page 13, line 3; page 14, lines 20-27; page 20, lines 15-22. The Examiner objected to the specification because it contains embedded hyperlink and/or other form of browser-executed code. The specification has been amended to delete the embedded hyperlink and/or other form of browser-executable code. As such, objection to the specification is obviated.

I. THE INVENTION

The present invention relates, in part, to isolated nucleic acid molecules, vectors and host cells, that comprise a nucleic acid sequence that encodes SGT4 proteins that are involved in signal transduction mechanisms. The claimed nucleic acid molecules can be used in a variety of applications, given their similarity in structure with genes comprising leucine rich repeat domain (LRR). The claimed nucleic acid molecules are homologous to the LRR portion of the Ras-suppressor protein-1 (RSU-1) and the flightless-I protein (FLI-1). LRR has been shown to interact with Ras both in vitro and in vivo in yeast. The nucleic acid molecules of the present invention are especially useful as reagents, e.g., as polynucleotide probes or PCR (polymerase chain reaction) primers which can be used for detecting any genes that contain LRR (including RSU-1, FLI-1 and SGT4) in chromosome mapping, Southern analyses, Northern analyses, and *in situ* hybridization assays. Moreover, the SGT4 proteins, nucleotides, peptides, antibodies, antagonists may be used to regulate the function or expression of SGT4 or genes containing LRR.

II. THE REJECTION UNDER 35 U.S.C. § 101 IS IN ERROR

Claims 1-6, 8, and 21 are rejected by the Examiner under 35 U.S.C. § 101 as allegedly lacking specific (or well-established) and substantial utility. The Examiner states:

> "The specification teaches . . . novel human polynucleotides, referred to collectively as SGT4, which encode proteins involved in signal transduction mechanisms. The invention is based . . . SGT4 shares substantial sequence homology with lucine rich repeat domain (LRRs) containing proteins, particularly Ras suppressor protein 1 (RSU-1) and flightless-1 protein homolog, but its primary sequence is unique. The expression of SGT4 is detected in various human tissues, and at particular high levels in skeletal muscle and heart. The specification discloses the sequences of SGT4 and variants; however, it fails to disclose the functional aspect of SGT4, its specific/particular role in

the asserted signal transduction mechanism. In view that the biological role of flightless-1 is still unknown (Fong et al., 1999, Genomics 58:146-157), and in view of the fact that the primary sequence of SGT4 is unique, it is unclear what is the role of SGT4 in the signal transduction mechanism. Thus, the specific utility is not well established."

Applicants respectfully disagree. Claims 1-6, 8, and 21 recite isolated nucleic acid molecules, vectors and host cells that comprises a nucleic acid sequence that encodes a gene comprising LRR domains. Applicants submit that the utilities provided in the specification, *inter alia*, on page 27, line 4 to page 28, line 18; page 33, line 10 to page 34, line 29; page 48, line 26 to page 49, line 12 for the claimed invention, for example, in providing probes for identification of genes comprising LRR domains; in providing host cells that express genes that comprise LRR domains and generation of antibodies against genes comprising LRR domains, in particular, RSU-1 and FLI-1 for use in diagnostic assays are sufficient to meet the requirements of 35 U.S.C. § 101.

According to the Examination Guidelines for the Utility Requirement, if the applicant has asserted that the claimed invention is useful for any particular practical purpose (*i.e.*, it has a "specific and substantial utility") and the assertion would be considered credible by a person of ordinary skill in the art, the Examiner should not impose a rejection based on lack of utility (66 F. R. 1098, Jan. 5, 2001).

Support of the assertion that the claimed nucleic acid molecules have specific utility is based on the presence in the claimed nucleic acid molecule of the LRR domain that is present in many proteins that function in the ras signal-transduction pathway. LRR has been shown to interact with Ras both in vitro, and in vivo in yeast (Shima et al., 2000, Mol Cell Biol 20(1): 26-33 ("Shima et al., 2000"; Reference AJ); Field et al., 1990, Science 247:464-466 ("Field et al., 1990"; Reference AG); and Suzuki et al., 1990, Proc. Natl. Acad. Sci. USA 87:8711-8715 ("Suzuki et al., 1990"; Reference AK). Applicants submit herewith as Exhibit D, an amino acid sequence comparison which shows that SGT4, (SEQ ID NO:3) shares 34% amino acid sequence identity and 52% amino acid sequence conservation with the LRR domain of human RSU-1. In addition, SGT4 (SEQ ID NO:3) shares 30% amino acid sequence identity and 53% amino acid sequence conservation with the LRR domain of human FLI-1, see Exhibit E. Applicants point out that this high percentage homology among LRRs of various LRR-containing genes are comparable to the alignment of the LRR domains of FLI-1 and RSU-1, which reveals 53% amino acid conservation and 35% amino acid identity (Claudianos et al., 1995, Mol. Biol. Evol. 12(3): 405-414; Reference AE). RSU-1

and FLI-1 have both been shown to suppress v-Ras transformation of cells. Rsu-1 has been shown to suppress the v-Ras-transformed phenotype and inhibits growth in both fibroblasts and epithelial cells (Cutler et al., 1993, Mol. Cell Biol. 12:3750-3756; Reference AF; Tsuda and Cutler, 1993, Genomics 18:461-462; Reference AL). Thus, Applicants submit that one skilled in the art would recognize that the claimed nucleic acid molecules encode a protein that is involved in suppressing transformation by activated Ras.

A number of genes also produced high similarity scores with SGT4. These include the *Fli-1* gene of other non-human species and other LRR containing genes such as *C. elegans Fli-1* (28% amino acid identity; 51% amino acid conservation with SGT4); yeast *Saccharomyces cerevisiae* adenylate cyclase (32% amino acid identity; 53% amino acid conservation with SGT4) and *S. kluyveri* adenylate cyclase (28% amino acid identity; 51% amino acid conservation with SGT4) (Kataoka et al., 1985, Cell 43:493-505). The LRRs of *S. cerevisiae* adenylate cyclase have been shown to be regulatory regions involved in Ras signal transduction (Shima et al., 2000; Field et al., 1990; Suzuki et al., 1990). This is consistent with the disclosures in the specification, *inter alia*, at page 5, lines 19-22, which states that SGT4 shares substantial sequence homology with LRR containing proteins, particularly RSU-1 and FLI-1 proteins. Hence, based on the high degrees of amino acid sequence identity and conservation between the LRR domain of the claimed nucleic acid molecules to the LRR domains of RSU-1, FLI-1 and other LRR containing genes that were shown to be involved in Ras signal transduction, Applicants submit that one of ordinary skill in the art would recognize that the claimed nucleic acid molecules encode a protein that is involved in signal transduction as asserted in the specification.

Moreover, the LRR domains of various proteins share a unique amino acid motif that is involved in ras signal transduction pathway. In general, the LRR domain contains a 23 amino acid motif, XxαXXLXXLXXLD/NLSXNXαXXαP (where α indicates an aliphatic amino acid and X is any amino acid). Applicants submit herewith as Exhibit F an alignment of SEQ ID NOS:1 and 3 with the translated human ras suppressing protein (RSU-1), mouse ras suppressing protein (RSP-1), together with LRR regions of human, Drosophila, and *Caenorhabditis elegans* FLI-1 proteins and yeast (*Saccharomyces cerevisiae* and *S. kluyveri*) adenylate cyclases. The alignment highlights similar LRR regions which are implicated in Ras signal transduction. Multiple aligned LRRs are indicated between arrowheads at amino acids 34-56, 57-79, 80-102, 103-127, 128-150, 151-173, and 174-196 (+ indicates conservative amino acid replacements). The conservation of the amino acid

residues within the LRR module, which is the 23-amino acid motif, reinforces that SGT4 has functions similar to that of the related ras signal transducing LRR domain of RSU-1, FLI-1 and other LRR domain containing proteins. As discussed in a peer-reviewed article, Claudiano et al. stated that the conservation of the amino acid residues of the LRR module is consistent with an emerging theme for the LRR domains of various genes in the signal transduction pathway.

Furthermore, as discussed above, the LRR domain has been shown to interact with ras both in vitro, and in vivo in yeast. Genetic and biochemical studies demonstrated that the LRR domain contains a binding site for the GTP-bound Ras (Minato et al., 1994, J. Biol. Chem. 269:20845-20851; Reference AH; Shima et al., 1997, Mol. Cell. Biol. 17:1057-1064; Vojtek et al., 1993, Cell 74:205-214; Reference AM). Based on (i) the high percentage amino acid sequence identity and conservation of SGT4 among other members of proteins containing LRR domains and (ii) the conservation of amino acid residues of the LRR module in organisims as distantly related over evolutionary time as *Homo sapiens*, *Drosophila melanogaster*, and *Caenorhabditis elegans,* one of skill in the art would recognize that the biological role of LRR domain containing genes are likely to be very similar. Thus, it is more likely than not that the skilled person would conclude that the proteins encoded by the claimed nucleic acid molecules also function as a protein in signal transduction pathway like the Ras pathway.

Further support for the function of SGT4 is provided in the reference Fong et al. cited by the Examiner. The Examiner alleges that the biological role of flightless-1 is still unknown citing Fong et al., 1999, Genomics 58:146-157 ("Fong et al."). Fong et al. teaches the identification of two related genes that encode proteins that interact with the LRR domain of human FLI-1 using the yeast two-hybrid system. Fong et al. at 146. Fong et al. further teaches that on the basis of sequence similarities among the LRR domains of proteins, FLI-1 belongs to a subclass that binds to GTPase-like signaling molecules. Fong et al. at page 147 citing Claudianos et al. Hence, Fong et al. a peer-reviewed article supports the teachings in the present invention that the SGT4 gene, which comprises the LRR domain, based on the sequence similarities among the LRR domains of various proteins, has a role in signal transduction. The Examiner is reminded that credibility of any utility is assessed from the perspective of one of ordinary skill in the art in view of the disclosure or any other evidence of record.

In conclusion, by comparing the amino acid sequence identity within the LRR domain among various proteins, one of skill in the art will certainly recognize that the LRR domain of SGT4 is highly homologous to the LRR domains of FLI-1 and RSU-1. Based on the conservation of the amino acid residues of the LRR module, one of skill in the art would conclude that the nucleotide sequences of SGT4 as set forth in SEQ ID NOS:1 and 3 encode proteins containing a LRR domain and, it is more likely than not, that these proteins are involved in signal transduction pathway. As such, the present nucleic acid molecules of the invention have specific utility.

The Examiner alleges that specific utility is not well established because the specification fails to disclose the functional aspect of SGT4, its specific/particular role in the asserted signal transduction mechanism. Under the Examination Guidelines for the Utility Requirement, actual demonstration of the functional activity of the claimed nucleic acid molecules is not necessary to establish a specific utility. That the particular biological/physiological function of the protein has not been identified or characterized does not negate the utility of the invention. As asserted in the specification, the claimed nucleic acid molecules can be used as probes in hybridization assays, for example, in Southern blot analysis to detect not only SGT4 but also any genes containing LRR domains, particularly, FLI-1 and RSU-1; in Northern blots to determine the level of expression of SGT4 or any genes containing LRR domains, in tissues or cell lines; in situ hybridization or PCR (see, for example, page 51, lines 10-14). Since the claimed polynucleotides are homologous to LRR, they may be used as a probe or a marker for the entire family of genes containing LRR and not just SGT4 if the stringency of the hybridization conditions is adjusted. These assays may be used to measure the expression of SGT4s encoded by nucleic acid molecules either of the invention or homologous to that of the invention. These analyses including the use of low stringency hybridization conditions are routinely performed by one of skill in the art. Since the described nucleic acid sequences can be used requiring if any, only routine laboratory procedures, no undue experimentation would be required to use the sequences as disclosed in the specification. Thus, the claimed sequences have a substantial and credible utility that is both described and fully enabled by the specification. In contrast to a general utility where any polynucleotide may be used as a gene probe or chromosome marker without specifying a DNA target, Applicants submit that the utility of the claimed polynucleotide is indeed specific because not every piece of polynucleotide in the genome may be used as a probe or a marker for genes containing LRRs, for example, FLI-1 and RSU-1. Hence, the claimed

sequences of the present invention may be used as a gene probe or chromosome marker, not for a non-specific target, but for a specific target, namely, genes containing LRRs, such as, FLI-1 and RSU-1. As such, the present polynucleotides have a specific, substantial and credible utility.

The Examiner further alleges the claimed invention does not have utility because the specification fails to disclose which disease or symptom is associated with SGT4 deficiency, nor has any evidence showed that a nutritional supplement with SGT4 would correct a nutritional deficiency.

As readily appreciated by one of skill in the art and disclosed in the present specification, genes containing LRRs, in particular, FLI-1 and RSU-1 are involved in a wide variety of roles in the body including, but not limited to, regulation of the signal transduction pathways. As disclosed in the specification, *inter alia*, at page 48, line 26 to page 49, line 12, SGT4 plays an important role in signal transduction mechanisms which regulate various aspects of cellular physiology, including cell survival, proliferation and differentiation. Thus abnormalities in these mechanisms can lead to a variety of pathological or abnormal conditions. Interfering with, neutralizing, or enhancing SGT4 functions can affect a wide variety of physiological changes. Accordingly, one of skill in the art would consider that the utility asserted by the Applicants would be specific and substantial.

The Examiner states that since the claimed invention is not supported by a specific and substantial utility, credibility of any utility cannot be assessed. As stated in the Examination Guidelines for the Utility Requirement, credibility is assessed from the perspective of one of ordinary skill in the art in view of the disclosure or any other evidence of record. Applicants submit that based on the high percentage amino acid sequence identity and conservation of SGT4 among other members of proteins containing LRR domains, location of the LRR domain at the amino-terminal, and interaction of LRR with ras both in vitro, and in vivo in yeast, conservation of the amino acid residues of the LRR module in distantly related organisms, one of skill in the art would recognize that the nucleic acid molecules of the present invention encode proteins that regulate a signal transduction pathway. Hence, not only do the nucleic acid molecules of the present invention have specific utilities, their utilities are credible and practical.

Since the polynucleotides of the present invention as described in claims 1, 2 and 3 have specific, substantial and credible utility, a vector comprising the polynucleotides,

host cell comprising the vector and method of producing the polypeptide as described in claims 4-6, 8, and 21 also have utility.

In view of the foregoing, Applicants submit that the claimed invention has specific, substantial and credible utility. Thus, Applicants respectfully request that the rejection of claims 1-6, 8, and 21 under 35 U.S.C. § 101 be withdrawn.

III. THE REJECTIONS UNDER 35 U.S.C. § 112, FIRST PARAGRAPH SHOULD BE WITHDRAWN

Claims 1-6, 8, and 21 are rejected under 35 U.S.C. § 112, first paragraph, as allegedly lacking utility. The Federal Circuit and its predecessor have determined that the utility requirement of Section 101 and the how to use requirement of Section 112, first paragraph, have the same basis – the disclosure of a credible utility. *See In re Brana*, 51 F.3d 1560, 1564, 34 USPQ2d 1436, 1441 (Fed. Cir. 1995); *see also In re Jolles*, 628 F.2d 1322, 1326 n.11, 206 USPQ 885, 889 n. 11 (CCPA 1980); and *In re Fouche*, 439 F.2d 1237, 1243, 169 USPQ 429, 434 (CCPA 1971). Applicants traverse this rejection on the ground that Claims 1-6, 8, and 21 have significant patentable utility as discussed in Section II, above. Applicants submit that when an Applicant satisfactorily rebuts a rejection based on a lack of utility under 35 U.S.C. § 101, the corresponding rejection imposed under 35 U.S.C. § 112, first paragraph, should also be withdrawn. Applicants submit that claims 1-6, 8, and 21 satisfy the utility requirement under 35 U.S.C. § 112, first paragraph. Thus, Applicants respectfully request that the rejection of Claims 1-6, 8, and 21 under 35 U.S.C. § 112, first paragraph, be withdrawn.

Claims 1, 3-6, 8, and 21 are also rejected under 35 U.S.C. § 112, first paragraph, because, allegedly, the specification has not provided an adequate written description of and has not conveyed that at the time of filing applicants were in possession of a representative number of nucleic acid molecules having the property of hybridizing under stringent conditions to SEQ ID NOS:1 or 3. Furthermore, the Examiner alleges that these claims embrace a large number of polynucleotides, which encode a protein that may or may not function as signal transduction proteins. The Examiner further alleges that the specification fails to provide an adequate written disclosure for all polynucleotides encompassed by the claims and their functional characteristics, whether any fragments or complements would also function as full length SEQ ID NO: 1 or 3. Applicants respectfully

disagree and, for the reasons discussed below, submit that the full scope of the pending claims is described in the specification.

The Guidelines to the Examination of Patent Applications Under 35 U.S.C. § 112, first paragraph for Written description provides:

> "To satisfy the written description requirement, a patent specification must describe the claimed invention . . . . using . . . structures . . . and formulas that fully set forth the claimed invention. Possession may be shown . . . including . . . actual reduction to practice . . . or by disclosure of drawings or structural chemical formulas . . . or by describing distinguishing identifying characteristics sufficient to show that the applicant was in possession of the claimed invention."

(66 F.R. 1104-1106, Jan. 5, 2001)

First, with respect to claim 1, Applicants submit that the specification provides adequate written description for the claimed nucleic acid molecules. Amended claim 1 is directed to an isolated nucleic acid molecule that comprises at least 50 contiguous bases of SEQ ID NO:1 or 3. There is no recitation in claim 1 that requires the claimed molecule to hybridize to another molecule. Applicants submit that the structure of the claimed nucleic acid molecules is well defined by the minimum length of the nucleic acid molecule, and by the nucleic acid sequence of the nucleic acid molecule. The claimed nucleic acid molecule comprises essentially a subsequence of SEQ ID NO:1 or 3 which are fully described in the specification at page 11, lines 19-27. Although the number of species in the claimed genus of nucleic acid molecule is large, based on the structural description in the specification, one of ordinary skill in the art can literally recite the sequences of every one of the nucleotide sequences that the claimed molecule comprises. As such, Applicants submit that the skilled person would immediately know from the specification that Applicants possess the invention of claim 1.

Amended claim 3 is directed to nucleic acid molecules comprising a nucleotide sequence that is at least 50 contiguous bases and that hybridizes to a completely defined nucleic acid molecule consisting of the nucleic acid sequence of SEQ ID NO:1 or 3 or a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO:2 or 4. The nucleic acid molecules are required to be of a minimum size and possess the identifying characteristics of hybridizing under a clearly articulated set of stringency conditions. Such a distinguishing identifying property of the claimed nucleic acid molecule are fully described in the specification (*see* page 11, line 19 to page 13, line 3).

The Guidelines to the Examination of Patent Applications Under 35 U.S.C.

§ 112, first paragraph for Written description states that :

> Factors to be considered in determining whether there is sufficient evidence of possession include the level of skill and knowledge in the art, partial structure, functional characteristics alone or coupled with a known or disclosed correlation between structure and function, and the method of making the claimed invention. Disclosure of any combination of such identifying characteristics that distinguish the claimed invention from other materials and would lead one of skill in the art to the conclusion that the applicant was in possession of the claimed species is sufficient.

Applicants submit that the correlation between nucleic acid sequence homology and hybridization conditions are very well understood by one of skill in the art; the skill and knowledge in the molecular biology arts is very high; and one of the characteristics of the nucleic acid molecule recited in the claims is essentially a test based on hybridization for distinguishing the claimed molecule from other materials. Furthermore, the claimed nucleic acid molecules can readily be synthesized chemically or produced using recombinant DNA techniques that are routine in the art. Applicants submit that based on a combination of structural and functional identifying characteristics and teachings on how to make and use the claimed nucleic acid molecules, one of skill in the art would draw the conclusion that the applicants were in possession of the claimed nucleic acid molecules.

Moreover, Applicants submit that possession of a representative number of the claimed nucleic acid molecules have been shown by actual reduction to practice. As discussed in the specification, *inter alia*, on page 5, lines 6-11, SEQ ID NOS: 1 and 3 are nucleotide sequences of SGT4-1 and SGT4-2, exemplary species within the claimed genus of nucleic acid molecules. One of skill in the art would readily recognize that nucleic acid molecules comprising any one of these SEQ IDs would hybridize under the stated stringency conditions to the defined nucleotide sequences as recited in the claims. Thus, the specification indeed provide representative examples of nucleic acid molecules that are encompassed by the genus of nucleic acid molecule of Claim 3.

Contrary to the Examiner's assertion that the claims encompass variants which encode proteins that may lack the functional activities of a signal transduction protein, Applicants respectfully point out that description of a biological function of a protein encoded by the nucleic acid molecule of claim 3 is not an absolute requirement for an adequate written description under 35 U.S.C. §112, first paragraph. As discussed in Section II, even though the biological function of the protein products may not be fully characterized, the claimed nucleic acid molecules themselves still have a useful function, such as, use as probes in

hybridization assays to determine expression of SGT4 and genes containing LRR domain, in particular, FLI-1 and RSU-1 in Northern blot analysis or in situ.

In view of the foregoing, Applicants submit that claims 1, 3-6, 8, and 21 satisfy the requirement under 35 U.S.C. § 112, first paragraph. Applicants submit that the specification provides adequate written description of the claimed invention.

The Examiner further alleges that the specification fails to provide an enabling disclosure for what such polynucleotides would comprise and how one would use such polynucleotides. Applicants respectfully disagree and, for the reasons discussed below, submit that the full scope of the pending claims is enabled by the specification.

The specification teaches and it is routine in the art to make polynucleotides containing or hybridizing under stringency conditions to the elected nucleic acid sequence of SEQ ID NOS:1 and 3. For example, the specification, *inter alia*, on page 5, line 28 to page 8, line 28 teaches how to use the nucleic acid molecule as a hybridization probe or a PCR primer to identify sequences containing the nucleic acid sequence and/or hybridizing to the nucleic acid sequence under stringency conditions in cDNA or genomic libraries. The specification, *inter alia*, on page 10, lines 11-15; page 18, lines 28-30 further teaches that polynucleotides of the inventions can also be synthesized chemically using methods that are routine in the art. Additionally, for example, the specification teaches how to identify certain variants of the nucleic acid sequence that are within the scope of the invention (*see, e.g.*, specification on page 13, lines 21-27 which describes identification of allelic and species variations). It is also well within the skill in the art to generate such polynucleotides that contain and/or hybridize to the particular nucleotide sequences using recombinant DNA techniques, methods for chemically synthesizing polynucleotides, PCR, etc. Accordingly, the skilled artisan could, in light of the specification and what was well known in the art, make the claimed polynucleotides.

Moreover, as discussed in Section II, *supra*, the specification does teach how to use the claimed polynucleotides. The specification teaches that the claimed polynucleotides can be put to a variety of practical uses. Although, as the Office Action points out, the biological function of the protein encoded by any specific fragment or hybridization variant is not known, the claimed polynucleotide sequences themselves, regardless of the function of the protein product, still have a useful function. The nucleic acid sequences, as well as fragments of the nucleic acid sequences would hybridize to human chromosome locations that represent SGT4 genes and genes containing LRR domains, in particular, FLI-1 and RSU-1; a transcribed

signal transduction protein mRNA, and its corresponding cDNA. By virtue of this correspondence with SGT4 genes and genes containing LRR domains, in particular, FLI-1 and RSU-1 on respective locations on the human chromosome or in a transcribed mRNA, the claimed sequences can be used as described in the specification, particularly, for chromosome mapping and marking for LRR domain containing genes.

The specification provides detailed teachings as to how to use the claimed polynucleotide in the above-listed methods. An invention is enabled even though the disclosure may require some routine experimentation to practice the invention. *Hybridtech Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 1384, 231 U.S.P.Q. 81, 94 (Fed. Cir. 1986). Employing the claimed sequences in these methods requires only routine experimentation that is well within the skill in the art using methodology either taught by the specification and/or routine in the art. Thus, the specification also enables the skilled artisan how to use the claimed sequences.

As the specification teaches how to make and to use the claimed polynucleotides, Applicants submit that claims 1, 3-6, 8, and 21 satisfy the requirement under 35 U.S.C. § 112, first paragraph. Applicants submit that the full scope of the claims are enabled.

V. THE REJECTIONS UNDER 35 U.S.C. §102 ARE OBVIATED

Claims 1, 3-6, and 21 are rejected under 35 U.S.C. § 102(a) as allegedly being anticipated by Zhao et al., (EST database)("Zhao"). The Examiner asserts that Zhao teaches isolated nucleic acids comprising at least 24 nucleotides of SEQ ID NO: 1 or 3, complement thereof; or an isolated nucleic acid molecule that hybridizes under stringent condition to SEQ ID NO: 1 or 3; an expression vector comprising the nucleic acid molecule and a host cell comprising the vector. Zhao discloses two nucleic acid molecules having accession numbers AQ427239 and AQ427288 in the EST database, which contain at least 24 contiguous bases of SEQ ID NOS:1 or 3, respectively, and which share sequence homology with the recited sequence ranging from 85.2-100%. It is well-settled law that, in order to anticipate under 35 U.S.C. § 102, a reference must teach all elements and limitations of the claimed invention. "Invalidity for anticipation requires that all of the elements and limitations of the claim are found within a single prior art reference". *Scripps Clinic & Research Foundation v. Genentech Inc.* 18 USPQ2d 1001, 1010 (Fed. Cir. 1991).

In response, Applicants have amended claim 1 to recite an isolated nucleic acid molecule that comprises at least 50 contiguous bases of SEQ ID NO:1 or 3. Applicants have also amended claim 3 to recite an isolated nucleic acid molecule which comprises a nucleotide sequence that is at least 50 contiguous bases and that hybridizes to a second nucleic acid molecule consisting of: (a) the nucleic acid sequence of SEQ ID NO:1 or 3; or (b) a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO:2 or 4. Zhao only teaches 41 contiguous bases of SEQ ID NO:1. Zhao does not teach a nucleic acid molecule that comprises at least 50 contiguous bases and that hybridizes to a nucleic acid molecule consisting of the nucleic acid sequence of SEQ ID NO:1 or 3; or (b) a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO:2 or 4. As such, rejection of claims 1, 3-6, 8, and 21 under 35 U.S.C. § 102(a) are obviated.

Claims 1, 3-6, 8, and 21 are rejected under 35 U.S.C. § 102(a) as allegedly being anticipated by Carninci et al., 1999, Methods in Enzymol 303:19-44 ("Carninci"). The Examiner asserts that Carninci teaches isolated nucleic acids, having the accession number AK010252 in the EST database, comprising at least 24 nucleotides of SEQ ID NO:1 or 3, which shares sequence homology with the recited sequences ranging from 72.8-83%, thus could hybridize with said sequences. Applicants have amended claims 1 and 3 as discussed above. Carninci does not teach a nucleic acid molecule that comprises at least 50 contiguous bases and that hybridizes to a nucleic acid molecule consisting of the nucleic acid sequence of SEQ ID NO:1 or 3; or (b) a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO:2 or 4. Carnici only teaches 38 contiguous bases of SEQ ID NO:3. As such, claims 1, 3-6, 8, and 21 are no longer anticipated by Carninci.

Since neither Zhao nor Carninci, teach or suggest each and every element of amended claims 1, 3-6, and 21, these references do not anticipate claims 1, 3-6, and 21. Applicants request that the rejections of claims 1, 3-6, and 21 under 35 U.S.C. § 102 be withdrawn.

CONCLUSION

Applicants respectfully request that the above-made remarks and amendments be entered and made of record in the file history of the instant application. An early allowance of the application is earnestly requested. If any issues remain in connection herewith, the Examiner is respectfully invited to telephone the undersigned to discuss the same.

Respectfully submitted,

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Laura A. Coruzzi 30,742
Laura A. Coruzzi (Reg. No.)
PENNIE & EDMONDS
1155 Avenue of the Americas
New York, New York 10036-2711
(212) 790-9090

By: 40,258
T. Christopher Tsang